```
==============================================================
Sequence Listing could not be accepted due to errors.
See attached Validation Report.
If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).
Reviewer: Anne Corrigan
Timestamp: Thu Jun 14 16:36:05 EDT 2007
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*************************************************************
Reviewer Comments:
<110>  Wei. Xin Gariepy .Jean
<130> LIBRARY OF HETEROMERIC TOXIN NIUTANTS, AND METHODS OF USING SAME

<140>  10598965
<141>  2007-06-13
<170> Patentln version 3.2.
<?lo> 1 d11> 299
<312> PRT
<2 13> Escherichia coli
<220>
<221> misc-feature
<223> Wild type SI-T-1 A chain
Ile Glu Gly Arg Ala Ser Lys Glu Phe Thr Leu Asp Phe Ser Thr Ala
1 5 10 15

The <130> response should go on the <120> line: the <130> line is for
the file reference, usually the docket number.

The above numeric identifiers (e.g., <?lo> are samples of globally
invalid numeric identifiers and text.  Please do not use tab codes
between amino acid numbers.  Please check the Sequence Rules for valid
format.
*************************************************************
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Application No: 10598965   Version No: 1.0

Input Set:

Output Set:

Started:	2007-06-13 17:25:27.911
Finished:	null
Elapsed:	null
Total Warnings:	2
Total Errors:	16
No. of SeqIDs Defined:	0
Actual SeqID Count:	2

Error code	Error Description
E 249	Order Sequence Error <110> -> <130>; Expected Mandatory Tag: <120> in Header
E 249	Order Sequence Error <170> -> <312>; Expected Mandatory Tag: <210> in Header
E 287	Invalid WIPO ST.2 date format; Use (YYYY-MM-DD) in <312> in SEQ
E 249	Order Sequence Error <312> -> <220>; Expected Mandatory Tag: <400> in Header
E 257	Invalid sequence data feature in <221> in SEQ ID (0)
E 249	Order Sequence Error <223> -> <210>; Expected Mandatory Tag: <400> in Header
E 212	Invalid Sequence ID Number; Expected 1 as next SeqID but skipped
E 249	Order Sequence Error <212> -> <223>; Expected Mandatory Tag: <213> in SEQID (2)
E 202	Invalid input format; Value must be an integer in <400> SEQID: (2)
E 254	The total number of bases conflicts with running total Input: 0, Calculated : 1 SEQID(2)
E 253	The number of bases differs from <211> Input: 32 Calculated:1
W 213	Artificial or Unknown found in <213> in SEQ ID (3)
E 254	The total number of bases conflicts with running total Input: 0, Calculated : 31 SEQID(3)
W 112	Upper case found in data; Found at position(31) SEQID(3)
E 254	The total number of bases conflicts with running total Input: 0, Calculated : 32 SEQID(3)
E 254	The total number of bases conflicts with running total, Input: 4,

```
          Input Set:


          Output Set:



            Started:   2007-06-13 17:25:27.911
           Finished:   null
            Elapsed:   null
     Total Warnings:   2
       Total Errors:   16
No. of SeqIDs Defined:   0
  Actual SeqID Count:   2
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Error code   Error Description

E   253   The number of bases differs from <211> Input: 31 Calculated:37

E   249   Order Sequence Error <212> -> <220>; Expected Mandatory Tag: <213>
            in SEQID (3)

<110> Wei. Xin Gariepy .Jean

<130> LIBRARY OF HETEROMERIC TOXIN NIUTANTS, AND METHODS OF USING SAME

<140> 10598965

<141> 2007-06-13

<170> Patentln version 3.2.

<?lo> 1 d11> 299

<312> PRT

<2 13> Escherichia coli

<220>

<221> misc-feature

<223> Wild type SI-T-1 A chain

Ile Glu Gly Arg Ala Ser Lys Glu Phe Thr Leu Asp Phe Ser Thr Ala

1 5 10 15

Lys Thr Tyr Val Asp Ser Leu Asn Val Ile Arg Ser Ala lle Gly Thr

30 25 3 0

Pro Leu Gln Thr lle Ser Ser Gly Gly Thr Ser Leu Leu Met Ile Asp

35 40 45

Ser Gly Ser GIy Asp Asn Leu Phe Ala Val Asp Val Arg Gly Ile Asp

50 5 5 60

Pro Glu Glu Gly Arg Phe Asn Asn Leu Arg Leu lle Val Glu Arg Asn

65 70 75 80

Asn Leu Tyr Val Thr Gly Phe Val Asn Arg Thr Asn Asn Val Phe Tyr 85 90 95

Arg Phe Ala Asp Phe Ser His Val Thr Phe Pro Gly Thr Thr Ala Val 100 105 110

Thr Leu Ser Gly Asp Ser Ser Tyr Thr Thr Leu Gln Arg Val Ala Gly 115 120 125

Ile Ser Arg Thr Gly Met Gln Ile Asn Arg His Ser Leu Thr 'Thr Ser 130 135 140

Tyr Leu Asp Leu Met Ser His Ser Gly Thr Ser Leu Thr Gln Ser Val 145 150 155 160

Ala Arg Ala Met Leu Arg Phe Val Thr Val Thr Ala Glu Ala Leu Arg 165 170 175

Phe Arg Gln Ile Gln Arg Gly Phe Arg Thr Thr Leu Asp Asp Leu Ser 1 SO 185 190

Gly Arg Ser Tyr Val Met Thr Ala Glu Asp Val Asp Leu Thr Leu Asn 195 200 205

Trp Gly Arg Leu Ser Ser Val Leu Pro Asp Tyr His Gly Gln Asp Ser 210 315 320

Val Arg Val Gly Arg lle Ser Phe Gly Ser Ile Asn Ala Ile Leu Gly

225 230 235 240

Ser Val Ala Leu Ile Leu Asn Cys His His His Ala Ser Arg Val Ala 245 250 355

Arg Met Ala Ser Asp Glu Phe Pro Ser Met Cys Pro Ala Asp Gly Arg

Val Arg Gly Ile Thr His Asn Lys lle Leu Trp Asp Sel- Ser I'hr Leu 275 280 285

Gly Ala Ile Leu Met Arg Arg Thr Ile Ser Ser 290 295

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<211> 32

<212> DNA

<2 13> Ai-tif'icial

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<223> Primer

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e

<210> 3

<211> 31

<212> DNA

<213> Artificial

<220>

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<400> 3

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L

<?lo> 4

<211> 302

<212> PRT

<2 13> Artificial

<220>

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His His Ile Glu Gly 1 5 10 15

Arg Ala Ser Lys Glu Phe Thr Leu Asp Phe Ser Thr Ala Lys 'Thr Tyr 20 25 30

Val Asp Ser Leu Asn Val lle Arg Ser Ala Ile Gly Thr Pro Leu Gln 35 40 4 5

Thr Ile Ser Ser Gly Gly Thr Ser Leu Leu Met Ile Asp Ser Gly Ses 5 0 5 5 60

Gly Asp Asn Leu Phe Ala Val Asp Val Arg Gly Ile Asp Pro Glu Glu 65 70 75 8 0

Gly Arg Phe Asn Asn Leu Arg Leu Ile Val Glu Arg Asn Asn Leu Tyr 85 90 95

Val Thr Gly Phe Val Asn Arg Thr Asn Asn Val Phe Tyr Arg Phe Ala 100 105 110

Asp Phe Ser His Val Thr Phe Pro Gly Thr Thr Ala Val Thr Leu Ser 115 120 125

Gly Asp Ser Ser Tyr Thr Thr Leu Gln Arg Val Ala Gly Ile Ser Arg 130 135 140

Thr Gly Met Gln lle Asn Arg His Ser Leu 'Thr Thr Ser Tyr Leu Asp

145 150 155 160

Leu Met Ser His Ser Gly Thr Ser Leu Thr Gln Ser Val Ala Arg Ala

165 170 175

Met Leu Arg Phe Val Thr Val Thr Ala Glu Ala Leu Arg Phe Arg Gln

Ile Gln Arg Gly Phe Arg Thr Thr Leu Asp Asp Leu Ser Gly Arg Ser 195 200 205

Tyr Val Met Thr Ala Glu Asp Val Asp Leu Thr Leu Asn TIT GIy Arg 2 10 215 220

Leu Ser Sel– Val Leu Pro Asp Tyr His Gly Gln Asp Ser Val Arg Val 225 230 235 240

Gly Arg Ile Ser Phe Gly Ser lle Asn Ala Ile Leu Gly Ser Val Ala 34 5 250 255

Leu Ile Leu Asn Cys His His His Ile Tyr Ser Asn Lys Leu Met Ala 260 265 270

Ser Arg Val Ala Arg Met Ala Ser Asp Glu Phe Pro Ser Met Cys Pro 275 280 285

Ala Asp Gly Arg Val Arg Gly Ile Thr His Asn Lys Ile Leu 290 295 300

<210> 5

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<212> PRT

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<220>

<233> SLT-1 A Chain lib#5 protein sequence (SAMS)

Lys Gly Met Arg Ser His His His His His His His His Ile Glu GIy 1 5 10 15

Arg Ala Ser Lys Glu Phe Thr Leu Asp Phe Ser Thr Ala Lys Thr Tyr 20 2 5 3 0

Val Asp Ser Leu Asn Val Ile Arg Ser Ala Ile Gly Thr Pro Leu Gln 35 40 45

Thr Ile Ser Ser Gly Gly Thr Ser Leu Leu Met Ile Asp Ser Gly Ser 5 0 5 5 60

Gly Asp Asn Leu Phe Ala Val Asp Val Arg Gly Ile Asp Pro Glu Glu 6 5 70 75 8 0

Gly Arg Phe Asn Asn Leu Arg Leu Ile Val Glu Arg Asn Asn Leu Tyr 8 5 90 9 5

Val Thr Gly Phe Val Asn Arg Thr Asn Asn Val Phe Tyr Arg Phe Ala 100 105 110

Asp Phe Ser His Val Thr Phe Pro Gly Thr Thr Ala Val Thr Leu Ser 115 120 125

Gly Asp Ser Ser Tyr Thr Thr Leu Gln AI–g Val Ala Gly Ile Ser Arg 130 135 140

Thr Gly Met Gln Ile Asn Arg His Ser Leu Thr Thr Ser Tyr Leu Asp

145 150 155 160

Leu Met Ser His Ser Gly Thr Ser Leu Thr Gln Ser Val Ala Arg Ala 165 170 175

Met Leu Arg Phe Val Thr Val Thr Ala Glu Ala Leu Arg Phe Asg Gln 180 185 190

Ile Gln Arg Gly Phe Arg Thr Thr Leu Asp Asp Leu Ser Gly Ars Ser

Tyr Val Met Thr Ala Glu Asp Val Asp Leu Thr Leu Asn Trp Gly Arg 2 10 215 220

Leu Ser Ser Val Leu Pro Asp Tyr His Gly Gln Asp Ser Val Arg Val 225 230 235 240

Gly Arg Ile Ser Phe Gly Ser Ile Asn Ala Ile Leu Gly Ser Val Ala 245 250 255

Leu Ile Leu Asn Cys His His His Ala Ala Phe Ala Asp Leu Ile Ala 260 265 270

Ser Arg Val Ala Arg Met Ala Ser Asp Glu Phe Pro Ser Met Cys Pro 275 280 285

Ala Asp Gly Arg Val Arg Gly Ile Thr His Asn Lys lle Leu Trp Asp 290 295 300

Ser Ser Thr Leu Gly Ala Ile Leu Met Arg Arg Thr Ile Ser Ser

305 310 315

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<211> 7

<212> PRT

<213> Artificial

<220>

<223> First melanoma active insert

Ile Tyr Ser Asn Lys Leu Met 1 5

<?lo> 7

<211> 7

<212> PRT

<2 13> Artificial

<220>

<223> Second melanoma active insert

Ala Ala Phe Ala Asp Leu Ile 1 5